

SEQUENCE LISTING

T0150  
*b2*  
(1) GENERAL INFORMATION:

- (i) APPLICANT: Caras, Ingrid W
- (ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 1 DNA Way
- (C) CITY: South San Francisco
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 94080

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/635130
- (B) FILING DATE: 19-Mar-1996
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Torchia, PhD., Timothy E.
- (B) REGISTRATION NUMBER: 36,700
- (C) REFERENCE/DOCKET NUMBER: P1001

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650/225-8674
- (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1877 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Extra Cellular Domain
- (B) LOCATION: 244-899
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: Transmembrane Domain
- (B) LOCATION: 901-978
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: signal peptide
- (B) LOCATION: 244-321
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GNCTAGAAC TAGTGGATCC CCCCCGGGCTG CAGGAATTCC GACGGCCCCT 50  
GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCAGGGCACAG 100  
CAGGAAGCAG GTCCCGGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150  
CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGGCGAC 200  
TTTGGGGGAG TTGGTGCCCC GCCCCCCAGG CCTTGGCGGG GTC ATG 246  
Met  
1  
5  
10  
285  
Gly Pro Pro His Ser Gly Pro Gly Val Arg Val Gly  
15  
20  
25  
324  
GCC CTG CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG Ala Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly  
30  
35  
40  
363  
CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys  
45  
50  
402  
AGG TTC CAG GCA GAG GGT GGT TAT GTG CTG TAC CCT CAG Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln

ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441  
Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg  
55 60 65

CCT CCT GGC CCT CAC TCC TCT CCT AAT TAT GAG TTC TAC 480  
Pro Pro Gly Pro His Ser Ser Pro Asn Tyr Glu Phe Tyr  
70 75

AAG CTG TAC CTG GTA GGG GGT GCT CAG GGC CGG CGC TGT 519  
Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg Arg Cys  
80 85 90

GAG GCA CCC CCT GCC CCA AAC CTC CTT CTC ACT TGT GAT 558  
Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp  
95 100 105

CGC CCA GAC CTG GAT CTC CGC TTC ACC ATC AAG TTC CAG 597  
Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln  
110 115

GAG TAT AGC CCT AAT CTC TGG GGC CAC GAG TTC CGC TCG 636  
Glu Tyr Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser  
120 125 130

CAC CAC GAT TAC TAC ATC ATT GCC ACA TCG GAT GGG ACC 675  
His His Asp Tyr Tyr Ile Ile Ala Thr Ser Asp Gly Thr  
135 140

CGG GAG GGC CTG GAG AGC CTG CAG GGA GGT GTG TGC CTA 714  
Arg Glu Gly Leu Glu Ser Leu Gln Gly Gly Val Cys Leu  
145 150 155

ACC AGA GGC ATG AAG GTG CTT CTC CGA GTG GGA CAA AGT 753  
Thr Arg Gly Met Lys Val Leu Leu Arg Val Gly Gln Ser  
160 165 170

CCC CGA GGA GGG GCT GTC CCC CGA AAA CCT GTG TCT GAA 792  
Pro Arg Gly Gly Ala Val Pro Arg Lys Pro Val Ser Glu  
175 180

ATG CCC ATG GAA AGA GAC CGA GGG GCA GCC CAC AGC CTG 831  
Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser Leu  
185 190 195

GAG CCT GGG AAG GAG AAC CTG CCA GGT GAC CCC ACC AGC 870  
Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser  
200 205

AAT GCA ACC TCC CGG GGT GCT GAA GGC CCC CTG CCC CCT 909  
Asn Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro  
210 215 220

CCC AGC ATG CCT GCA GTG GCT GGG GCA GCA GGG GGG CTG 948  
Pro Ser Met Pro Ala Val Ala Gly Ala Ala Gly Gly Leu  
225 230 235

GCG CTG CTC TTG CTG GGC GTG GCA GGG GCT GGG GGT GCC 987  
Ala Leu Leu Leu Gly Val Ala Gly Ala Gly Gly Ala  
240 245

ATG TGT TGG CGG AGA CGG CGG GCC AAG CCT TCG GAG AGT 1026  
Met Cys Trp Arg Arg Arg Ala Lys Pro Ser Glu Ser  
250 255 260

VB2 CGC CAC CCT GGT CCT GGC TCC TTC GGG AGG GGA GGG TCT 1065  
Arg His Pro Gly Pro Gly Ser Phe Gly Arg Gly Gly Ser  
265 270

CTG GGC CTG GGG GGT GGA GGT ATG GGA CCT CGG GAG 1104  
Leu Gly Leu Gly Gly Gly Met Gly Pro Arg Glu  
275 280 285

GCT GAG CCT GGG GAG CTA GGG ATA GCT CTG CGG GGT GGC 1143  
Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly  
290 295 300

GGG GCT GCA GAT CCC CCC TTC TGC CCC CAC TAT GAG AAG 1182  
Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys  
305 310

GTG AGT GGT GAC TAT GGG CAT CCT GTG TAT ATC GTG CAG 1221  
Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln  
315 320 325

GAT GGG CCC CCC CAG AGC CCT CCA AAC ATC TAC TAC ACA 1260  
Asp Gly Pro Pro Gln Ser Pro Pro Asn Ile Tyr Tyr Thr  
330 335

TCG ATT TCT GTG TTG GAG TGG CCC ATA TTG CAT ACG ATA 1299  
Ser Ile Ser Val Leu Glu Trp Pro Ile Leu His Thr Ile  
340 345 350

CAA CTG TTT TTC ATG CGA TCC AAG TGC TCC CGT GTC ACT 1338  
Gln Leu Phe Phe Met Arg Ser Lys Cys Ser Arg Val Thr  
355 360 365

ACA TTC TTA TTT CCT GTG CAA GTT ATT ACG ACA TCG ACT 1377  
Thr Phe Leu Phe Pro Val Gln Val Ile Thr Thr Ser Thr  
370 375

TGC CGG ATG ACT TCA TTT AGC TTT ACC ACC CTG AAC CCA 1416  
Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn Pro  
380 385 390

TCC ATG CAG GCC TGC AGA GCA CAG ATG GGG GAA TTC CGA 1455  
Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg  
395 400

ATC AGA TGG TGT TTC TGG GGG GAC AGG ATC CTG GGT ACG 1494  
Ile Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr  
405 410 415

GCT CTG TTT GTG CTT GTG CTT ATT CTT CTT CTT GGG AGG 1533  
Ala Leu Phe Val Leu Val Ile Leu Leu Leu Gly Arg  
420 425 430

CTG AAT ATG CAT CAG ACG ACA CTG CTC CGG CAA CGG GCC 1572  
Leu Asn Met His Gln Thr Thr Leu Leu Arg Gln Arg Ala  
435 440

AGT GTG GAG GCG GAA GCC GGC CAG CAT GGT CCC CTG TG 1610  
Ser Val Glu Ala Glu Ala Gly Gln His Gly Pro Leu  
445 450 455

ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG 1660

GAGGCTGCTG TTATCATGGG AACCAGGCAG ATCAATCATC CCTGGCAGGT 1710

CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAATTAA 1760

TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTG TGCTGCCTGT 1810

CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGGATTGCA TATCAAGCTT 1860

ATCGATAACCG TCGACCT 1877

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 455 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly Ala  
1 5 10 15

Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly Leu Ser Leu  
20 25 30

Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys Arg Phe Gln Ala Glu  
35 40 45

Gly Gly Tyr Val Leu Tyr Pro Gln Ile Gly Asp Arg Leu Asp Leu  
50 55 60

Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn  
65 70 75

Tyr Glu Phe Tyr Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg  
80 85 90

Arg Cys Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp  
95 100 105

Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln Glu Tyr  
110 115 120

Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser His His Asp Tyr  
125 130 135

Tyr Ile Ile Ala Thr Ser Asp Gly Thr Arg Glu Gly Leu Glu Ser  
140 145 150

Leu Gln Gly Gly Val Cys Leu Thr Arg Gly Met Lys Val Leu Leu  
155 160 165

Arg Val Gly Gln Ser Pro Arg Gly Gly Ala Val Pro Arg Lys Pro  
170 175 180

Val Ser Glu Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser  
185 190 195

Leu Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser Asn  
200 205 210

Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro Pro Ser Met  
215 220 225

Pro Ala Val Ala Gly Ala Ala Gly Gly Leu Ala Leu Leu Leu Leu  
230 235 240

Gly Val Ala Gly Ala Gly Gly Ala Met Cys Trp Arg Arg Arg Arg  
 245 250 255  
 Ala Lys Pro Ser Glu Ser Arg His Pro Gly Pro Gly Ser Phe Gly  
 260 265 270  
 Arg Gly Gly Ser Leu Gly Leu Gly Gly Gly Gly Met Gly Pro  
 275 280 285  
 Arg Glu Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly  
 290 295 300  
 Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys Val Ser  
 305 310 315  
  
 Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln Asp Gly Pro Pro  
 320 325 330  
 Gln Ser Pro Pro Asn Ile Tyr Tyr Thr Ser Ile Ser Val Leu Glu  
 335 340 345  
 Trp Pro Ile Leu His Thr Ile Gln Leu Phe Phe Met Arg Ser Lys  
 350 355 360  
 Cys Ser Arg Val Thr Thr Phe Leu Phe Pro Val Gln Val Ile Thr  
 365 370 375  
 Thr Ser Thr Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn  
 380 385 390  
 Pro Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg Ile  
 395 400 405  
 Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr Ala Leu Phe  
 410 415 420  
 Val Leu Val Leu Ile Leu Leu Gly Arg Leu Asn Met His Gln  
 425 430 435  
 Thr Thr Leu Leu Arg Gln Arg Ala Ser Val Glu Ala Glu Ala Gly  
 440 445 450  
 Gln His Gly Pro Leu  
 455

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 2380 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GNCTAGAAN TAGTGGATCC CCCCAGGCTG CAGGAATTCC GACGGCCCCT 50  
GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCAGGGCACAG 100  
CAGGAAGCAG GTCCCGGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150  
CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200  
TTTGGGGGAG TTGGTGCCCC GCCCCCCCAGG CCTTGGCGGG GTCATGGGGC 250  
CCCCCCATTC TGGGCCGGGG GGCGTGCAG GTCGGGGCCCT GCTGCTGCTG 300  
GGGGTTTTGG GGCTGGTGTG TGGGCTCAGC CTGGAGCCTG TCTACTGGAA 350  
CTCGGCGAAT AAGAGGTTCC AGGCAGAGGG TGGTTATGTG CTGTACCCCTC 400  
AGATCGGGGA CCGGCTAGAC CTGCTCTGCC CCCGGGCCCG GCCTCCTGGC 450  
CCTCACTCCT CTCCTAATTA TGAGTTCTAC AAGCTGTACC TGGTAGGGGG 500  
TGCTCAGGGC CGGCGCTGTG AGGCACCCCC TGCCCCAAC CTCCTCTCA 550  
CTTGTGATCG CCCAGACCTG GATCTCCGCT TCACCATCAA GTTCCAGGAG 600  
TATAGCCCTA ATCTCTGGGG CCACGAGTTC CGCTCGCACC ACGATTACTA 650  
CATCATTGCC ACATCGGATG GGACCCGGGA GGGCCTGGAG AGCCTGCAGG 700  
GAGGTGTGTG CCTAACCCAGA GGCATGAAGG TGCTTCTCCG AGTGGGACAA 750  
AGTCCCCGAG GAGGGGCTGT CCCCCGAAAA CCTGTGTCTG AAATGCCCAT 800  
GGAAAGAGAC CGAGGGCAG CCCACAGCCT GGAGCCTGGG AAGGAGAACCC 850  
TGCCAGGTGA CCCCCACCAGC AATGCAACCT CCCGGGGTGC TGAAGGCCCC 900  
CTGCCCCCTC CCAGCATGCC TGCAGTGGCT GGGGCAGCAG GGGGGCTGGC 950  
GCTGCTCTTG CTGGCGTGG CAGGGGCTGG GGGTGCCATG TGTTGGCGGA 1000

GACGGCGGGC CAAGCCTCG GAGAGTCGCC ACCCTGGTCC TGGCTCCTTC 1050  
GGGAGGGGAG GGTCTCTGGG CCTGGGGGGT GGAGGTGGGA TGGGACCTCG 1100  
GGAGGCTGAG CCTGGGGAGC TAGGGATAGC TCTGCAGGGT GGCGGGCTG 1150  
CAGATCCCCC CTTCTGCCCC CACTATGAGA AGGTGAGTGG TGACTATGGG 1200  
CATCCTGTGT ATATCGTGCA GGATGGGCC CCAGAGGCC CTCCAAACAT 1250  
CTACTACAAG GTATGAGGGC TCCTCTCACG TGGCTATCCT GAATCCAGCC 1300  
CTTCTTGGGG TGCTCCTCCA GTTTAATTCC TGGTTTGAGG GACACCTCTA 1350  
ACATCTCGGC CCCCTGTGCC CCCCCAGCCC CTTCACTCCT CCCGGCTGCT 1400  
GTCCTCGTCT CCACTTTAG GATTCCCTAG GATTCCCCT GCCTTACTTC 1450  
CTGCCCTCCC GTTTGGCCAT GGGTGCCCCC CTCTGTCTCA GTGTCCCTGG 1500  
ATCCTTTTC CTTGGGGAGG GGCACAGGCT CAGCCTCCTC TCTGACCATG 1550  
ACCCAGGCAT CCTTGTCCCC CTCACCCACC CAGAGCTAGG GGCGGAACA 1600  
GCCCACCTTT TGGTTGGCAC CGCCTTCTTT CTGCCTCTCA CTGGTTTCT 1650  
CTTCTCTATC TCTTATTCTT TCCCTCTCTT CCGTCTCTAG GTCTGTTCTT 1700  
CTTCCCTAGC ATCCTCCTCC CCACATCTCC TTTCACCCCTC TTGGCTTCTT 1750  
ATCCTGTGCC TCTCCCCTCT CCGGGTGGG GGCATCAAAG CATTTCTCCC 1800  
CTTAGCTTTC AGCCCCCTT CTGACCTCTC ATACCAACCA CTCCCCTCAG 1850  
TCTGCCAAAA ATGGGGCCT TATGGGAAG GCTCTGACAC TCCACCCAG 1900  
CTCAGGCCAT GGGCAGCAGG GCTCCATTCT CTGGCCTGGC CCAGGCCTCT 1950  
ACATACTTAC TCCAGCCATT TGGGGTGGTT GGGTCATGAC AGCTACCATG 2000  
AGAAGAAGTG TCCCGTTTG TCCAGTGGCC AATAGCAAGA TATGAACCGG 2050  
TCGGGACATG TATGGACTTG GTCTGATGCT GAATGGCCA CTTGGGACCG 2100  
GAAGTGACTT GCTCCAGACA AGAGGTGACC AGGCCCGGAC AGAAATGGCC 2150  
TGGGAAGTAG CAGAAGCAGT GCAGCAGGAA CTGGAAGTGC CTTCATCCAG 2200

GACAGGAAGT AGCACTTCTG AAACAGGAAG TGGTCTGGCT GGAACCTCAA 2250  
GTGGCTTAGT CTGGGGGATC AGGAGGTGGG AGGTGGATGG TTCTTATTCT 2300  
GTGGAGAAGA AGGGCGGGAA GAACTTCCTT TCAGGAGGAA GCTGGAACTT 2350  
ACTGACTGTA AGAGGTTAGA GGTGGACCGA 2380

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly Ala  
1 5 10 15  
Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly Leu Ser Leu  
20 25 30  
Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys Arg Phe Gln Ala Glu  
35 40 45  
Gly Gly Tyr Val Leu Tyr Pro Gln Ile Gly Asp Arg Leu Asp Leu  
50 55 60  
Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn  
65 70 75  
Tyr Glu Phe Tyr Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg  
80 85 90  
Arg Cys Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp  
95 100 105  
Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln Glu Tyr  
110 115 120  
Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser His His Asp Tyr  
125 130 135  
Tyr Ile Ile Ala Thr Ser Asp Gly Thr Arg Glu Gly Leu Glu Ser  
140 145 150

L<sup>e</sup>u Gln Gly Gly Val Cys Leu Thr Arg Gly Met Lys Val Leu Leu  
155 160 165  
Arg Val Gly Gln Ser Pro Arg Gly Gly Ala Val Pro Arg Lys Pro  
170 175 180  
Val Ser Glu Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser  
185 190 195  
Leu Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser Asn  
200 205 210  
Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro Pro Ser Met  
215 220 225  
Pro Ala Val Ala Gly Ala Ala Gly Gly Leu Ala Leu Leu Leu Leu  
230 235 240  
Gly Val Ala Gly Ala Gly Gly Ala Met Cys Trp Arg Arg Arg Arg  
245 250 255  
Ala Lys Pro Ser Glu Ser Arg His Pro Gly Pro Gly Ser Phe Gly  
260 265 270  
Arg Gly Gly Ser Leu Gly Leu Gly Gly Gly Gly Met Gly Pro  
275 280 285  
Arg Glu Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly  
290 295 300  
Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys Val Ser  
305 310 315  
Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln Asp Gly Pro Pro  
320 325 330  
Gln Ser Pro Pro Asn Ile Tyr Tyr Lys Val  
335 340

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 454 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCCGACGCTG TGAGGCACCC CCTGCCCAA ACCTCCTTCT CACTTGTGAT 50  
CGCCCAGACC TGGATCTCCG CTTCACCATC AAGTTCCAGG AGTATAGCCC 100  
TAATCTCTGG GGCCACGAGT TCCGCTCGCA CCACGATTAC TACATCATTG 150  
CCACATCGGA TGGGACCCGG GAGGCCTGGG AGAGCCTGCA GGGAAAGTGTG 200  
TGCCTAACCA GAGGCATGAA GGTGCTTCTC CGAGTNNGAC AAAGTCCCGA 250  
GGAGGGGCTG TCCCCCGAAA ACCTGTGTCT GAAATGCCA TGGAAAGAGA 300  
CCGAGGGGCA GCCCACAGCC TGGGAGCCTG GGGAAAGGAGA ACCTGCCAGG 350  
TGACCCCACC AGCAATNCAA CCTTCCGGGG TTGCTTGAAG GGCCCCTTGA 400  
CCCTTCCCA GCATTGCNTG CANTTGGTTN GGGCAGCAN GGGGGNGTTT 450  
TGGC 454

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGACAAAGTC CCGAGGAGGG GCTGTCCCCC GAAAACCTGT GTCTGAAATG 50

CCCATGGAAA 60

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTTCTCC TTCCCCAGGC TCCCAGGCTG TGGGCTGCC CTCGGTCTCT 50

TTCCATGGGC 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Arg Pro Gly Gln Arg Trp Leu Gly Lys Trp Leu Val Ala  
1 5 10 15

Met Val Val Trp Ala Leu Cys Arg Leu Ala Thr Pro Leu Ala Lys  
20 25 30

Asn Leu Glu Pro Val Ser Trp Ser Ser Leu Asn Pro Lys Phe Leu  
35 40 45

Ser Gly Lys Gly Leu Val Ile Tyr Pro Lys Ile Gly Asp Lys Leu  
50 55 60

Asp Ile Ile Cys Pro Arg Ala Glu Ala Gly Arg Pro Tyr Glu Tyr  
65 70 75

Tyr Lys Leu Tyr Leu Val Arg Pro Glu Gln Ala Ala Ala Cys Ser  
80 85 90

Thr Val Leu Asp Pro Asn Val Leu Val Thr Cys Asn Arg Pro Glu  
95 100 105

Gln Glu Ile Arg Phe Thr Ile Lys Phe Gln Glu Phe Ser Pro Asn  
110 115 120

Tyr Met Gly Leu Glu Phe Lys Lys His His Asp Tyr Tyr Ile Thr  
125 130 135

Ser Thr Ser Asn Gly Ser Leu Glu Gly Leu Glu Asn Arg Glu Gly  
140 145 150

Gly Val Cys Arg Thr Arg Thr Met Lys Ile Ile Met Lys Val Gly  
155 160 165

Gln Asp Pro Asn Ala Val Thr Pro Glu Gln Leu Thr Thr Ser Arg  
170 175 180

Pro Ser Lys Glu Ala Asp Asn Thr Val Lys Met Ala Thr Gln Ala  
185 190 195

Pro Gly Ser Arg Gly Ser Leu Gly Asp Ser Asp Gly Lys His Glu  
200 205 210

Thr Val Asn Gln Glu Glu Lys Ser Gly Pro Gly Ala Ser Gly Gly  
215 220 225

Ser Ser Gly Asp Pro Asp Gly Phe Phe Asn Ser Lys Val Ala Leu  
230 235 240

Phe Ala Ala Val Gly Ala Gly Cys Val Ile Phe Leu Leu Ile Ile  
245 250 255

Ile Phe Leu Thr Val Leu Leu Leu Lys Leu Arg Lys Arg His Arg  
260 265 270

Lys His Thr Gln Gln Arg Ala Ala Ala Leu Ser Leu Ser Thr Leu  
275 280 285

Ala Ser Pro Lys Gly Gly Ser Gly Thr Ala Gly Thr Glu Pro Ser  
290 295 300

Asp Ile Ile Ile Pro Leu Arg Thr Thr Glu Asn Asn Tyr Cys Pro  
305 310 315

His Tyr Glu Lys Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile  
320 325 330

Val Gln Glu Met Pro Pro Gln Ser Pro Ala Asn Ile Tyr Tyr Lys  
335 340 345

Val  
346

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Val Arg Arg Asp Ser Val Trp Lys Tyr Cys Trp Gly Val  
1 5 10 15

Leu Met Val Leu Cys Arg Thr Ala Ile Ser Lys Ser Ile Val Leu  
20 25 30

Glu Pro Ile Tyr Trp Asn Ser Ser Asn Ser Lys Phe Leu Pro Gly  
35 40 45

Gln Gly Leu Val Leu Tyr Pro Gln Ile Gly Asp Lys Leu Asp Ile  
50 55 60

Ile Cys Pro Lys Val Asp Ser Lys Thr Val Gly Gln Tyr Glu Tyr  
65 70 75

Tyr Lys Val Tyr Met Val Asp Lys Asp Gln Ala Asp Arg Cys Thr  
80 85 90

Ile Lys Lys Glu Asn Thr Pro Leu Leu Asn Cys Ala Lys Pro Asp  
95 100 105

Gln Asp Ile Lys Phe Thr Ile Lys Phe Gln Glu Phe Ser Pro Asn  
110 115 120

Leu Trp Gly Leu Glu Phe Gln Lys Asn Lys Asp Tyr Tyr Ile Ile  
125 130 135

Ser Thr Ser Asn Gly Ser Leu Glu Gly Leu Asp Asn Gln Glu Gly  
140 145 150

Gly Val Cys Gln Thr Arg Ala Met Lys Ile Leu Met Lys Val Gly  
155 160 165

Gln Asp Ala Ser Ser Ala Gly Ser Thr Arg Asn Lys Asp Pro Thr  
170 175 180

Arg Arg Pro Glu Leu Glu Ala Gly Thr Asn Gly Arg Ser Ser Thr  
185 190 195

Thr Ser Pro Phe Val Lys Pro Asn Pro Gly Ser Ser Thr Asp Gly  
200 205 210

Asn Ser Ala Gly His Ser Gly Asn Asn Ile Leu Gly Ser Glu Val  
215 220 225

Ala Leu Phe Ala Gly Ile Ala Ser Gly Cys Ile Ile Phe Ile Val  
230 235 240

Ile Ile Ile Thr Leu Val Val Leu Leu Leu Lys Tyr Arg Arg Arg  
245 250 255

His Arg Lys His Ser Pro Gln His Thr Thr Thr Leu Ser Leu Ser  
260 265 270

Thr Leu Ala Thr Pro Lys Arg Ser Gly Asn Asn Asn Gly Ser Glu  
275 280 285

Pro Ser Asp Ile Ile Ile Pro Leu Arg Thr Ala Asp Ser Val Phe  
290 295 300

Cys Pro His Tyr Glu Lys Val Ser Gly Asp Tyr Gly His Pro Val  
305 310 315

Tyr Ile Val Gln Glu Met Pro Pro Gln Ser Pro Ala Asn Ile Tyr  
320 325 330

Tyr Lys Val  
333